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# OSTEOCLAST PROTON PUMP SUBUNIT

## RELATED APPLICATION

This application is a continuation of U.S. Application No. 08/605,378, filed February 22, 1996, the entire teachings of which are incorporated herein by reference.

## GOVERNMENT FUNDING

Work described herein was supported by NIH grant DE-07378 from the National Institute of Dental Research. The U.S. Government has certain rights in the invention.

## BACKGROUND OF THE INVENTION

Solubilization of bone mineral and degradation of the organic matrix of bone depends on the formation, by osteoclasts, of an acidic extracellular compartment.

Osteoclasts are multinucleated giant cells which are responsible for bone resorption and degrade both the inorganic and organic components of bone in a local area subjacent to the matrix attachment site (Blair *et al.*, *J. Cell Biol.*, *102*:1164-1172 (1986)). Dissolution of the hydroxyapatite mineral phase is dependent upon acidification of the subosteoclastic resorption lacuna, via the action of carbonic anhydrase II and a proton pump (Vaes, *J. Cell Biol.*, *39*:676-697 (1968); Baron *et al.*, J. Cell Biol., *101*: 2210-2222 (1985); and Blair and Schlesinger, in *Biology and Physiology of the Osteoclast*, Rifkin and Gay, eds. (CRC Press, Boca Raton), pp. 259-287 (1992)).

V-type proton pumps are multi-subunit complexes with two distinct functional domains: a peripherally-associated cytoplasmic catalytic sector that contains 70- (subunit A), 58- (subunit B), 40- and 33-kDa (subunit E) subunits (Xie and Stone, *J. Biol. Chem.*, *263*:9859-9866 (1988)), and a proton channel, which is likely composed of

116-, 39-, and 17-kDa components (Crider *et al., J. Biol. Chem., 269*:17379-17381 (1994)). Considerable speculation has focused on the possibility that osteoclast-specific proton pump subunits exist, particularly because a unique osteoclast mechanism might allow controlled and specific clinical intervention for bone mass disorders such as osteoporosis.

## SUMMARY OF THE INVENTION

The present invention pertains to a gene encoding a novel human 116-kDa polypeptide subunit of the osteoclast proton pump (OC-116KDa). OC-116KDa mRNA was found at high levels in giant cells of osteoclastomas by Northern analysis but was not detected in tumor stromal cells or in other tissues including kidney, liver, skeletal muscle and brain. OC-116KDa mRNA was localized to multinucleated giant cells within the osteoclastoma tumor by *in situ* hybridization. Analysis of the deduced amino acid sequence of the polypeptide indicates that it is a membrane bound protein with at least six transmembrane domains. Thus, it appears that OC-116kDa represents a novel human 116-kDa subunit of a proton pump which is expressed in osteoclasts in a cell-specific manner. The cell-specific expression of OC-116KDa makes it useful as a target for therapeutic intervention in diseases with increased resorption of bone or cartilage, such as osteoporosis and osteoarthritis.

Thus, the present invention relates to a gene encoding a polypeptide or protein which is a human osteoclast proton pump subunit. In a particular embodiment, the osteoclast proton pump subunit is a 116-kDa subunit. In another embodiment, the invention also relates to a gene encoding a polypeptide or protein which is an osteoclast proton pump subunit and comprising a nucleotide sequence of SEQ ID NO: 1. The invention described herein also relates to the polypeptide or protein encoded by the described genes. The invention also pertains to isolated DNA encoding a polypeptide which is an osteoclast proton pump subunit and comprising the nucleotide sequence of SEQ ID NO: 1 or its complementary sequence or DNA which hybridizes under conditions of medium to high stringency to the nucleotide sequence of SEQ ID NO: 1 or its complement. The invention further relates to isolated DNA encoding a polypeptide which is a human osteoclast proton pump subunit and which comprises the amino acid sequence of SEQ ID NO: 3 (Figure 2).

The invention described herein also relates to a novel polypeptide or protein which is a human 116-kDa proton pump subunit. The invention further relates to a

polypeptide or protein which is an osteoclast proton pump subunit and has the amino acid sequence of SEQ ID NO: 2. The invention also relates to a polypeptide or protein which is a human proton pump subunit and which comprises the amino acid sequence of SEQ ID NO: 3.

The present invention also relates to antibodies which bind a polypeptide which is a human osteoclast proton pump subunit. For instance, polyclonal and monoclonal antibodies which bind to the described polypeptides or proteins are within the scope of the invention. The invention also pertains to DNA constructs comprising DNA encoding a polypeptide which is an osteoclast proton pump subunit, as well as to host cells stably transformed or transfected with the DNA constructs of this invention.

The present invention also relates to assays for identifying agents which alter the rate of bone degradation. In particular, the agent to be tested is administered to a test subject or added to an *in vitro* cell culture, and the rate of bone degradation is determined and compared with the rate of bone degradation in a control subject or cell culture which has not been treated with the test agent. An increase or decrease in the rate of bone degradation in the test animal or cell culture indicates that the tested agent alters the rate of bone degradation.

The present invention also relates to methods of treating bone mass disorders characterized by an undesirably high rate of bone degradation, such as osteoporosis and osteoarthritis. In a particular embodiment, an agent which decreases the rate of bone degradation by decreasing the activity of a 116-kDa proton pump subunit (e.g., an antagonist of OC-116KDa) is administered in a therapeutically appropriate amount to a patient who has a detrimentally increased rate of bone degradation, thereby decreasing the patient's bone degradation rate.

The present invention also relates to methods of treating bone mass disorders characterized by an undesirably low rate of bone degradation. In a particular embodiment, an agent which increases the rate of bone degradation by increasing the activity of a 116-kDa proton pump subunit (e.g., an agonist of OC-116KDa) is administered in a therapeutically appropriate amount to a patient who has a detrimentally decreased rate of bone degradation, thereby increasing the patient's bone degradation rate. Alternatively, a polypeptide which is a human 116-kDa osteoclast proton pump subunit, optionally formulated with a physiologically appropriate medium, can be administered to a subject with a detrimentally decreased rate of bone degradation. The present invention also pertains to pharmaceutical compositions

comprising a polypeptide which is a human 116-kDa osteoclast proton pump subunit, or an agonist or antagonist thereof.

The polypeptides and proteins of the present invention also have utility as osteoclast cell surface markers. Expression of the described polypeptides or proteins is characteristic of osteoclasts, and is unlikely to be found in extracellular fluids such as blood, since the proteins are integral membrane proteins. Thus, these proteins can be labelled, e.g., radioactively or fluorescently, and used as cell surface markers for osteoclasts.

## BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B represent the nucleotide sequence (SEQ ID NO: 1) and deduced amino acid sequence (SEQ ID NO: 2) of human OC-116KDa.

Figure 2 illustrates the consensus amino acid sequence (SEQ ID NO: 3) resulting from an alignment of the amino acid sequences of human OC-116KDA, rat and bovine 116-kDa proton pump subunits. Gaps (indicated by dashes) were introduced to maximize alignment of the sequences.

## DETAILED DESCRIPTION OF THE INVENTION

Considerable effort has focused on the characterization of the special properties of the osteoclast proton pump. As described herein, a gene encoding a human 116-kDa polypeptide of the vacuolar proton pump, which appears to be uniquely expressed in osteoclast cells, has been isolated.

In order to solubilize bone mineral and degrade the organic matrix of bone, osteoclasts must secrete 1-2 protons for every $Ca^{2+}$ liberated. This transport is a major metabolic activity of osteoclasts and requires an electrogenic proton pump. The proton pump has not been purified in homogeneous form from mammalian osteoclast-ruffled membranes, and therefore its structure and biochemical properties have not yet been described in detail. Based upon immunological cross-reactivity, Blair *et al.* (Blair *et al.* (1989)) hypothesized that the osteoclast proton pump is a V-type proton pump. However, the osteoclast proton pump possesses several unique features, including a unique pharmacological profile; that is, the proton pump in osteoclast-derived membranes was not only shown to be sensitive to NEM and Bafilomycin A1, similar to the classical vacuolar proton pump, but also to be sensitive to vanadate, an inhibitor of P-type ATPase (Chatterjee *et al.*, *Proc. Natl. Acad. Sci. USA, 89*:6257-6261 (1992)).

Furthermore, the osteoclast proton pump is the most active of all acid transport systems studied. Some of these properties may be dependent upon the activity of the OC-116KDa subunit in osteoclasts.

As described herein, a gene encoding a novel human osteoclast proton pump 116-kDa subunit (OC-116KDa) has been identified by differential screening of a human osteoclastoma cDNA library. The primary structure of the 116-kDa polypeptide predicts a 822-residue protein composed of two large domains, each of which constitutes approximately half of the protein: a highly charged hydrophilic amino-terminal domain and a hydrophobic carboxyl terminal domain that contains multiple membrane-spanning regions. At least six transmembrane regions are present in the carboxyl-terminal half of the OC-116KDa polypeptide (Table 1), as judged by the criteria of Klein *et al.* (Klein *et al.*, *Biochem. Biophys. Acta.*, *815*:468-476 (1985)) and Kyte and Doolittle (Kyte and Doolittle, *J. Mol. Biol.*, *157*:105-132 (1982)).

Table 1

| No. | Sequence | Hydrophobicity | Residues |
|---|---|---|---|
| 1 | YTIITFPFLFAVMFGDVGHGLLMFLF ALAMVL SEQ ID NO: 4 | -2.96 | 391-422 |
| 2 | QTFFRGRYLLLLMGLFSIYTGFIYNE SEQ ID NO: 5 | -2.93 | 438-463 |
| 3 | MSVILGVVHMAFGVVLGVFNH SEQ ID NO: 6 | -2.81 | 537-558 |
| 4 | LPELTFLLGLFGYLVFLVIYKWLCV WAARA SEQ ID NO: 7 | -3.14 | 571-600 |
| 5 | QATLVVLALAMVPILLLGTPLHL SEQ ID NO: 8 | -3.34 | 632-653 |
| 6 | EVGVAAVVLVPIFAAFAVMTVAILL VMEGLSAF SEQ ID NO: 9 | -3.46 | 764-796 |

Approximately 12 x $10^3$ clones from a pcDNAII osteoclastoma library were replica-plated and were screened by differential hybridization using mixed cDNA probes derived by reverse transcription of mRNA from either the original osteoclastoma tumor (osteoclast+) or from propagated stromal cell mRNA (osteoclast-). As described previously (Li *et al., J. Bone Mine. Res., 10*:1197-1202 (1995)), 195 clones gave a positive hybridization signal with tumor cDNA, but were negative or very weakly positive with stromal cell cDNA. Of these 195 clones, 6 contained a novel human cathepsin (Li *et al.*, 1995), 14 clones contained inserts with a sequence identical to TRAP, and 77 clones encoded MMP-9 (92-kDa type IV collagenase) (Wucherpfennig *et al.* (1994)), all of which are markers of human osteoclasts.

In addition, one clone which gave a positive hybridization signal with tumor cDNA, but was negative with stromal cell cDNA, was found to possess approximately 60% homology to the rat 116-kDA vacuolar type proton pump subunit, but was not identical to any known proton pump subunit. This clone was designated OC-116KDa.

Northern analysis of mRNA from the osteoclastoma tumor using an $\alpha^{32}$P-labelled 1.0 kb 3' OC-116KDa cDNA probe revealed a transcript of approximately 2.7 kb. A 0.5 kb probe from the 5' end of OC-116 kDa gave the same result (data not shown). OC-116KDa mRNA was found at high levels in the osteoclastoma tumor, and at much lower levels in the human pancreatic adenocarcinoma cell line (AsPC-1), but was not detected in skeletal muscle, liver, kidney, or brain. OC-116KDa mRNA was also absent from osteoclastoma stromal cells, normal rat osteoblasts (ROB), as well as a panel of human cell lines: osteoblastic (HOS-TE85), myelomonocytic (U-937), T lymphocyte (HSB-2), epithelial (laryngeal carcinoma HEp-2), neuroblastoma (SK-N-MC), and normal skin fibroblasts (CRL 1467).

Rescreening the pcDNAII library failed to yield clones containing full-length inserts. A second library was therefore constructed in phage using the Lambda-ZAP system (Stratagene). This library consisted of ~6 x $10^5$ clones of average insert length 1.0 kb. Screening of this library yielded 25 positive clones, of which the two longest (p-18 and p-43) contained inserts of greater than 2.6 kb. Complete bidirectional sequence analysis was carried on the p-43 clone. Four other clones including p-18 were partially sequenced. All sequences were identical.

The nucleotide sequence (SEQ ID NO: 1) and the deduced amino acid sequence (SEQ ID NO: 2) of the OC-116KDa cDNA clone are shown in Figures 1A and 1B. The nucleotide sequence of the cDNA encoding the OC-116KDa proton pump polypeptide contains 2622 base pairs excluding the 3'-poly(A) tail. The cDNA contains a 57 base pair 5' untranslated region, and a rather short 3' untranslated region of 99 base pairs. The nucleotide sequence contains an open reading frame, starting from the first ATG codon, encoding an 822-amino acid polypeptide. The sequence context of the putative initiator methionine has a flanking sequence in agreement with the consensus sequences for an initiator methionine (1/G)CCATGG) (Kozak, *Nucleic Acids Res., 15*:8125-8148 (1987)). At the 3' end, the AATAAA sequence is a common polyadenylation signal. The cDNA is full-length as judged by the fact that its size corresponds well to the message size observed on RNA blots and that it contains an in-frame termination codon 5' to the initiator methionine. In addition, the cDNA sequence exhibits a single large open reading frame, the translation of which predicts the synthesis of an 822-amino acid protein.

Database searches revealed that OC-116KDa shows 59.4% homology at the nucleotide level with the rat 116-kDa subunit of the clathrin-coated vesicle proton

pump and 59.1% homology with the bovine brain 116-kDa subunit vacuolar proton pump. OC-116KDa exhibits 46.9% and 47.2% homology at the amino acid level with the rat 116KDa polypeptide and the bovine 116KDa polypeptide, respectively (Perin *et al., J. Biol. Chem. 266*:3877-3881 (1991); Peng *et al., J. Biol. Chem. 269*:17262-17266 (1994)).

The composition of OC-116KDa is characterized by an abundance of hydrophilic resides in the first 390 amino acids and a rather hydrophobic region in the following 432 amino acids. Hydrophobicity plots indicate that at least six transmembrane regions are present in the carboxyl-terminal portion of the molecule. The putative transmembrane regions are separated by spacer regions of different length and hydrophilicity (data not shown).

Based on the hydropathy plots, OC-116KDa shows structural homology with other 116KDa hydrophobic membrane proteins with transport-related function, including rat- and bovine-116KDa (Perin *et al.* (1991)). All three proteins are about 830 amino acids in length and contain six transmembrane domains with a hydrophilic region between domains. Figure 2 illustrates the consensus sequence obtained when the amino acid sequences of rat and bovine 116KDa are aligned with the amino acid sequence of OC-116KDa.

Cells within the osteoclastoma tumor which produce mRNA for OC-116KDa were identified by *in situ* hybridization. A digoxygenin-labelled antisense probe was strongly reactive with all multinucleated osteoclasts, but was unreactive with stromal cells. In contrast, the sense probe produced only minimal background staining, which was not localized to any cell type.

Since OC-116KDa appears to be a subunit of a V-type proton pump, the possibility that this molecule represents the human homolog of the brain-expressed rat and bovine 116KDa polypeptide was considered. However several lines of evidence argue against this possibility, and instead indicate that OC-116KDa represents a different gene. First, the structure of the classical 116-kDa subunits of V-type proton pumps are highly conserved. For example, the rat 116KDa polypeptide is 96.75% similar to the bovine 116KDa polypeptide at the amino acid level, whereas OC-116KDa had only about 47% homology to either the rat or bovine 116KDa polypeptide. Second, the full length mRNA of OC-116KDa is 2.7 kb, whereas both rat and bovine full length mRNAs for the 116-kDa subunits are 4.1 kb. Compared to rat and bovine 116KDa cDNAs, which contain a long 3' untranslated region (UTR) of 1321 base pairs, OC-

116KDa contains a rather short 3' untranslated region of 99 base pairs. The functional significance of this difference is unclear at this time. However, the 3' UTR has been found to affect the function of mRNAs in the cytoplasm in several ways. These include localization, control of mRNA stability, and regulation of translation efficiency (Decker and Parker, Current opinion in *Cell Biology, 7*:386-392 (1995)). These differences may constitute part of the molecular basis for the precise regulation of expression of the osteoclast proton pump during the bone remodeling process. Third, OC-116KDa mRNA was found at high levels in the osteoclastoma tumor but was not detected in other normal human tissues including kidney, brain, liver and skeletal muscle (data not shown). This is in contrast to the ubiquitous distribution of the rat and bovine 116-kDa subunit. Finally, OC-116KDa mRNA was localized to osteoclasts within the osteoclastoma tumor by *in situ* hybridization.

Interestingly, the amino acid sequence of OC-116KDa also exhibits 59% homology with Tj6, which is an immune suppressor and membrane binding protein described in the mouse (Lee *et al., Molecular Immunology, 27*:1137-1144 (1990)). The functional significance of this similarity is currently unclear.

Although the function of the 116-kDa subunit in the V-type proton pump is not definitively established, it appears to be an essential component of the vertebrate pumps (Wucherpfennig *et al., J. Bone Min. Res., 9*:549-556 (1994)), and is also present in lower unicellular eukaryotes and plants (Parry *et al., J. Biol. Chem. 264*:20025-20032 (1989); and Kane *et al., J. Biol. Chem. 264*:19236-19244 (1989)). In yeast, disruption by mutation of the gene encoding this subunit results conditional lethality at pH values of greater than 6.5 (Kane, *J. Exp. Biol. 172*:93-103 (1992); and Umemoto *et al., J. Biol. Chem. 266*:24526-24532 (1991)). The 17- and 116-kDa subunits are the components of the proton pump that are most hydrophobic (Arai *et al., J. Biol. Chem., 263*:8796-8802 (1988)). Based on hydrophilicity plots of the amino acid sequence, OC-116KDa shows structural homology with other 116-kDa proton pump subunits (data not shown) and also contains a large and highly charged amino-terminal domain of unknown function which may interact with the cytoplasmic catalytic sector. These data suggest that the OC-116KDa polypeptide may be part of the proton-conducting, intramembranous complex of the vacuolar proton pump, and may also play a role in mediating the coupling between ATP hydrolysis by the cytoplasmic 70- and 58-kDa subunits, and proton translocation by the intramembranous subunits, including perhaps its own transmembrane regions (Perin *et al.* (1991)).

It remains possible that osteoclasts contain two types of proton pumps, one utilizing OC-116KDa, and the other employing the classical 116-kDa subunit. Several pieces of data argue against this hypothesis. As shown by Chatterjee *et al.* (Chatterjee *et al.* (1992)), it is possible to completely inhibit proton transport with various inhibitors (NEM, Bafilomycin and vanadate) used separately, but there is only one $K_m$ for the presence of various concentrations of ATP in preparations of chicken osteoclasts. Second, a polyclonal antibody against the 116-kDa subunit of the clathrin-coated vesicle proton pump, which cross-reacts with the osteoclast proton pump, detects only one protein band at about 100kDa in Western blots of both the isolated osteoclast and clathrin-coated vesicle proton pumps (Mattsson *et al., J. Biol. Chem., 269*:24979-24982 (1994)).

Recently, alternative mRNA splicing was shown to generate tissue-specific isoforms of the 116-kDa subunit of the V-type proton pump in bovine brain (Peng *et al.* (1994)), and of the A subunit in chicken osteoclasts (Hermamdo *et al., PNAS 92*(13):6087-6091 (1995)). However, isoforms result from alternative mRNA splicing of same gene; that is, in the A isoform of the catalytic A subunit of the vacuolar proton pump in chicken osteoclasts, a 72-base pair cassette replaces a 90-base pair cassette present in the classical A1 isoform (Hermamdo *et al.* (1995)). Similarly, two distinct calcitonin receptors characterized from the giant cell tumor of bone differ from each other only by the presence or absence of a predicted 16-amino acid insert in the putative first intracellular domain (Gorn *et al., J. Clin. Invest., 95*:2680-2691 (1995)).

Taken together, these data demonstrate that OC-116KDa represents a novel 116-kDa subunit of a proton pump which is distinct from the previously-described 116-kDa subunit, and which is expressed at high levels in osteoclasts.

The present invention relates to a gene encoding a polypeptide or protein which is a human osteoclast proton pump subunit. In a particular embodiment, the osteoclast proton pump subunit is a 116-kDa subunit. In another embodiment, the invention also relates to a gene encoding a polypeptide or protein which is an osteoclast proton pump subunit and comprising a nucleotide sequence consisting of SEQ ID NO: 1; the invention described herein also relates to the polypeptide or protein encoded by the described genes. The invention also pertains to isolated DNA encoding a polypeptide which is an osteoclast proton pump subunit and comprising the nucleotide sequence of SEQ ID NO: 1 or its complementary sequence or DNA which hybridizes under conditions of medium to high stringency to the nucleotide sequence of SEQ ID NO: 1

or its complement. Stringency conditions which are appropriately termed "medium stringency" or "high stringency" are known to those skilled in the art or can be found in standard texts such as *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

The invention described herein also relates to a polypeptide or protein which is a human osteoclast proton pump subunit; in a particular embodiment, the polypeptide or protein is a 116-kDa proton pump subunit. In one embodiment, the polypeptide or protein which is an osteoclast proton pump subunit has the amino acid sequence of SEQ ID NO: 2.

The present invention also relates to antibodies which bind a polypeptide which is an osteoclast proton pump subunit. For instance, polyclonal and monoclonal antibodies which bind to the described polypeptide or protein are within the scope of the invention. A mammal, such as a mouse, hamster or rabbit, can be immunized with an immunogenic form of the polypeptide (i.e., an antigenic fragment of the polypeptide which is capable of eliciting an antibody response). Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. The protein or polypeptide can be administered in the presence of an adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibody.

Following immunization, anti-peptide antisera can be obtained, and if desired, polyclonal antibodies can be isolated from the serum. Monoclonal antibodies can also be produced by standard techniques which are well known in the art (Kohler and Milstein, *Nature 256*:495-497 (1975); Kozbar et al., *Immunology Today 4*:72 (1983); and Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96 (1985)).

The invention also provides expression vectors containing a nucleic acid sequence encoding a polypeptide which is a human osteoclast proton pump subunit operably linked to at least one regulatory sequence. "Operably linked" is intended to meant that the nucleotide sequence is linked to a regulatory sequence in a manner which allow expression of the nucleic acid sequence. Regulatory sequences are art-recognized and are selected to produce a polypeptide which is a human 116-kDa osteoclast proton pump subunit. Accordingly, the term "regulatory sequence" includes promoters, enhancers, and other expression control elements which are described in

Goeddel, *Gene Expression Technology: Methods in Enzymology 185*, Academic Press, San Diego, CA (1990). It should be understood that the design of the expression vector may depend on such factors as the choice of the host cell to be transformed and/or the type of protein desired to be expressed. For instance, the polypeptides of the present invention can be produced by ligating the cloned gene, or a portion thereof, into a vector suitable for expression in either prokaryotic cells, eukaryotic cells or both (see, for example, Broach, *et al.*, *Experimental Manipulation of Gene Expression*, ed. M. Inouye (Academic Press, 1983) p. 83; *Molecular Cloning: A Laboratory Manual*, 2nd Ed., ed. Sambrook *et al.* (Cold Spring Harbor Laboratory Press, 1989) Chapters 16 and 17).

Prokaryotic and eukaryotic host cells transfected by the described vectors are also provided by this invention. For instance, cells which can be transfected with the vectors of the present invention include, but are not limited to , bacterial cells such as *E. coli*, insect cells (baculovirus), yeast or mammalian cells such as Chinese hamster ovary cells (CHO).

Thus, a nucleotide sequence derived from the cloning of the osteoclast proton pump subunit polypeptides described herein can be used to produce a recombinant form of the protein via microbial or eukaryotic cellular processes. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial cells), are standard procedures used in producing other well known proteins. Similar procedures, or modifications thereof, can be employed to prepare recombinant proteins according to the present invention by microbial means or tissue-culture technology.

The present invention further relates to assays for identifying agents which alter the rate of bone degradation. As used herein, "alters" is intended to mean either increases or decreases. Also as used herein, an "agent" is intended to include, but is not limited to, peptides, drugs and small organic molecules. In particular, the agent to be tested is administered to a test animal or added to an *in vitro* cell culture, and the rate of bone degradation is determined and compared with the rate of bone degradation in a control animal or cell culture which has not been treated with the test agent. An increase or decrease in the rate of bone degradation in the test animal or cell culture indicates that the agent alters the rate of bone degradation. Thus, the present invention also pertains to agonists and antagonists of the OC-116KDa protein.

The present invention also relates to methods of treating bone mass disorders such as osteoporosis and osteoarthritis. In a particular embodiment, an agent which decreases the rate of bone degradation (e.g., an antagonist of OC-116KDa) is administered in a therapeutically appropriate amount to a patient who has a detrimentally increased rate of bone degradation, thereby decreasing the patient's bone degradation rate.

The present invention also relates to methods of treating bone mass disorders characterized by an undesirably low rate of bone degradation. In a particular embodiment, an agent which increases the rate of bone degradation by increasing the activity of a 116-kDa proton pump subunit (e.g., an agonist of OC-116KDa) is administered in a therapeutically appropriate amount to a patient who has a detrimentally decreased rate of bone degradation, thereby increasing the patient's bone degradation rate. Alternatively, a polypeptide which is a human 116-kDa osteoclast proton pump subunit, optionally formulated with a physiologically appropriate medium, can be administered to a subject with a detrimentally decreased rate of bone degradation.

The present invention also pertains to pharmaceutical compositions comprising a polypeptide which is a human 116-kDa osteoclast proton pump subunit, or an agonist or antagonist thereof. For instance, the polypeptide or protein of the present invention can be formulated with a physiologically acceptable medium to prepare a pharmaceutical composition. The particular physiological medium may include, but is not limited to, water, buffered saline, polyols (e.g., glycerol, propylene glycol, liquid polyethylene glycol) and dextrose solutions. The optimum concentration of the active ingredient(s) in the chosen medium can be determined empirically, according to procedures well known to medicinal chemists, and will depend on the ultimate pharmaceutical formulation desired. Methods of introduction of exogenous human osteoclast proton pump subunit polypeptides at the site of treatment include, but are not limited to, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, oral and intranasal. Other suitable methods of introduction can also include rechargeable or biodegradable devices and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The polypeptides and proteins of the present invention also have utility as osteoclast cell surface markers. Expression of the described polypeptides is

characteristic of osteoclasts, and is unlikely to be found in extracellular fluids such as blood, since the proteins are integral membrane proteins. Thus, these proteins can be labelled, e.g., radioactively or fluorescently, and used as cell surface markers for osteoclasts.

As used herein, terms are understood to have their art-recognized meaning unless otherwise defined. The teachings of references cited herein are hereby incorporated herein by reference.

The invention will be further illustrated by the following non-limiting exemplifications:

## Examples

### Cells and Cell Culture

Human osteoclastoma tumors, consisting of ~30% multinucleated tartrate resistant acid phosphatase positive (TRAP+) giant cells, were obtained courtesy of Dr. Andrew Rosenberg, Massachusetts General Hospital, Boston, MA. These multinucleated cells possess a closely similar phenotype to osteoclasts and are also capable of excavating resorption pits on bone slices (Horton and Helfrich, in *Biology and Physiology of the Osteoclast*, Rifkin and Gay, eds. (CRC Press, Boca Raton), pp. 33-53 (1992); and Flanagan *et al.*, *Cancer, 62*:1139-1145 (1988)). The remainder of the tumor consists of "stromal" cells, a mixture of cells types with fibroblastic/mesenchymal morphology. The osteoclastoma tumor was dissociated by a brief trypsinization and was placed into tissue culture in medium consisting of Dulbecco's Minimal Essential Medium. Disaggregated tumor cells were passaged weekly for 4 weeks, at which time all multinucleated, TRAP+ cells had disappeared, while the stromal cells continued to proliferate. Stromal cells were mononuclear, TRAP-, and variably alkaline phosphatase+.

Osteoblastic (HOS-TE85), myelomonocytic (U-937), T lymphocyte (HSB-2), neuroblastoma (SK-N-MC), pancreatic adenocarcinoma (AsPC-1) and normal skin fibroblast (CRL 1467) cell lines were purchased from ATCC, Bethesda, MD. The epithelial cell line Hep-2 was kindly provided by Dr. Margaret Duncan, Forsyth Dental Center. Normal rat osteoblasts (ROB) were obtained by sequential enzymatic digestion of fetal rat calvaria as described in Li *et al.* (Li *et al., Nucleic Acids Research, 23:*5064-5072 (1995)).

Library Construction and Differential Screening

Two human osteoclastoma cDNA libraries were prepared in pcDNAII vector (InVitrogen) and in the Lambda-ZAP system (Stratagene), and differential screening was performed as described in Li *et al.* (1995). Briefly, clones were randomly picked from the pcDNAII library and were hand plated in triplicate on nitrocellulose filters. Mixed cDNA probes were produced from mRNA isolated from the osteoclastoma tumor and from propagated stromal cells. The clones which were reactive with the tumor probe, but which were unreactive or only weakly reactive with the stromal cell probe were isolated. Purified DNA from these clones was rescreened in a dot blot format to confirm the original result.

cDNA Cloning and Sequencing

For full-length cDNA characterization, a 1.0 kb putative proton pump probe labelled with $\alpha^{32}$PdCTP was used to screen the Lambda-ZAP osteoclastoma library. Positive clones were purified, and the size of inserts was determined following excision with Kpn1 and Xbal. A clone containing a full-length insert of 2.6 kb was subjected to controlled digestion with ExoIII to generate a series of diminishing insert sizes. Sequence analysis was then carried out from both ends by the dideoxy method (Sanger *et al., Proc. Natl. Acad. Sci. USA, 74*: 5463-5467 (1977)) using the Sequenase kit (U.S. Biochemical Corp). Homologies were compared with known proton pump sequences using the BLAST program at the National Center for Biotechnology Information (N.C.B.I.).

Northern Blotting

Total RNA from osteoclastomas and cell lines was isolated by the method of Chomczynski and Sacchi (Chomczynski and Sacchi, *Analytical Biochemistry, 162*(1):156-159 (1987)). Whole cell RNA from human tissues was purchased from Clontech, Palto Alto, CA. Total cellular RNA was separated on a 1.0% agarose gel containing 6% formamide and transferred to nylon membranes. The integrity and quality of RNA was confirmed by ethidium bromide staining. Both 1.0 kb 3'-end and 0.5 kb 5'-end OC-116KDa cDNAs were used as probes. Probes were radiolabeled with $\alpha^{32}$pdCTP using a random primer labeling kit (Stratagene). Hybridization was performed as described previously in Li *et al.* (1995).

*In situ* Hybridization

*In situ* hybridization was performed as described in Li *et al.* (1995). Briefly, the 1.0 kb OC-116KDa insert was subcloned into pBluescript SK, and cDNA probes were generated from the T3 (sense) and T7 (antisense) promoters respectively. Probes were labelled with digoxygenin-UTP using the Genius System (Boehringer Mannheim) and developed with an alkaline phosphatase-labelled antibody. *In situ* hybridization was carried out on 7 mm cryostat sections of a human osteoclastoma. Hybridized probes were visualized immunologically with a digoxygenin-nucleic acid detection kit according to the manufacturer's instructions (Genius System, Boehringer Mannheim). Developed slides were photographed using a Nikon Diaphot microscope.

Equivalents

Those skilled in the art will recognize or be able to ascertain, using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed in the scope of the following claims.